

Rec'd PCT/PTO 24 FEB 2008

10/519328

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/519,328

Source:

Date Processed by STIC:

PT
2/24/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 02/24/2006

PATENT APPLICATION: US/10/519,328

TIME: 12:28:44

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\02242006\J519328.raw

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4 <110> APPLICANT: BOUGUELERET; Lydie
5   NIKNEJAD; Anne
7 <120> TITLE OF INVENTION: SECRETED PEPTIDES
10 <130> FILE REFERENCE: 4-33619A/GEP
12 <140> CURRENT APPLICATION NUMBER: 10/519,328
C--> 13 <141> CURRENT FILING DATE: 2004-12-23
15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/007069
16 <151> PRIOR FILING DATE: 2003-07-02
18 <150> PRIOR APPLICATION NUMBER: 60/393,840
19 <151> PRIOR FILING DATE: 2002-07-02
21 <160> NUMBER OF SEQ ID NOS: 10
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1821
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: PROPEP
32 <222> LOCATION: (1)...(1821)
33 <223> OTHER INFORMATION: Latent transforming growth factor-beta-binding
34   protein precursor 2
36 <221> NAME/KEY: SIGNAL
37 <222> LOCATION: (1)...(35)
38 <223> OTHER INFORMATION: Predicted by SignalP version 2.0
W--> 40 <221> SITE
41 <222> LOCATION: (96)...(97)
42 <223> OTHER INFORMATION: Dibasic peptidase cleavage site
W--> 44 <221> SITE
45 <222> LOCATION: (104)...(105)
46 <223> OTHER INFORMATION: Dibasic peptidase cleavage site
W--> 48 <221> SITE
49 <222> LOCATION: (113)...(114)
50 <223> OTHER INFORMATION: Dibasic peptidase cleavage site
W--> 52 <400> 1
53 Met Arg Pro Arg Thr Lys Ala Arg Ser Pro Gly Arg Ala Leu Arg Asn
54 -35 -30 -25 -20
55 Pro Trp Arg Gly Phe Leu Pro Leu Thr Leu Ala Leu Phe Val Gly Ala
56 -15 -10 -5
57 Gly His Ala Gln Arg Asp Pro Val Gly Arg Tyr Glu Pro Ala Gly Gly
58 1 5 10
59 Asp Ala Asn Arg Leu Arg Arg Pro Gly Gly Ser Tyr Pro Ala Ala Ala
60 15 20 25
61 Ala Ala Lys Val Tyr Ser Leu Phe Arg Glu Gln Asp Ala Pro Val Ala

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62 30          35          40          45
63 Gly Leu Gln Pro Val Glu Arg Ala Gln Pro Gly Trp Gly Ser Pro Arg
64          50          55          60
65 Arg Pro Thr Glu Ala Glu Ala Arg Arg Pro Ser Arg Ala Gln Gln Ser
66          65          70          75
67 Arg Arg Val Gln Pro Pro Ala Gln Thr Arg Arg Ser Thr Pro Leu Gly
68          80          85          90
69 Gln Gln Gln Pro Ala Pro Arg Thr Arg Ala Ala Pro Ala Leu Pro Arg
70          95          100          105
71 Leu Gly Thr Pro Gln Arg Ser Gly Ala Ala Pro Pro Thr Pro Pro Arg
72 110          115          120          125
73 Gly Arg Leu Thr Gly Arg Asn Val Cys Gly Gly Gln Cys Cys Pro Gly
74          130          135          140
75 Trp Thr Thr Ala Asn Ser Thr Asn His Cys Ile Lys Pro Val Cys Glu
76          145          150          155
77 Pro Pro Cys Gln Asn Arg Gly Ser Cys Ser Arg Pro Gln Leu Cys Val
78          160          165          170
79 Cys Arg Ser Gly Phe Arg Gly Ala Arg Cys Glu Glu Val Ile Pro Asp
80          175          180          185
81 Glu Glu Phe Asp Pro Gln Asn Ser Arg Leu Ala Pro Arg Arg Trp Ala
82 190          195          200          205
83 Glu Arg Ser Pro Asn Leu Arg Arg Ser Ser Ala Ala Gly Glu Gly Thr
84          210          215          220
85 Leu Ala Arg Ala Gln Pro Pro Ala Pro Gln Ser Pro Pro Ala Pro Gln
86          225          230          235
87 Ser Pro Pro Ala Gly Thr Leu Ser Gly Leu Ser Gln Thr His Pro Ser
88          240          245          250
89 Gln Gln His Val Gly Leu Ser Arg Thr Val Arg Leu His Pro Thr Ala
90          255          260          265
91 Thr Ala Ser Ser Gln Leu Ser Ser Asn Ala Leu Pro Pro Gly Pro Gly
92 270          275          280          285
93 Leu Glu Gln Arg Asp Gly Thr Gln Gln Ala Val Pro Leu Glu His Pro
94          290          295          300
95 Ser Ser Pro Trp Gly Leu Asn Leu Thr Glu Lys Ile Lys Lys Ile Lys
96          305          310          315
97 Ile Val Phe Thr Pro Thr Ile Cys Lys Gln Thr Cys Ala Arg Gly His
98          320          325          330
99 Cys Ala Asn Ser Cys Glu Arg Gly Asp Thr Thr Thr Leu Tyr Ser Gln
100          335          340          345
101 Gly Gly His Gly His Asp Pro Lys Ser Gly Phe Arg Ile Tyr Phe Cys
102 350          355          360          365
103 Gln Ile Pro Cys Leu Asn Gly Gly Arg Cys Ile Gly Arg Asp Glu Cys
104          370          375          380
105 Trp Cys Pro Ala Asn Ser Thr Gly Lys Phe Cys His Leu Pro Ile Pro
106          385          390          395
107 Gln Pro Asp Arg Glu Pro Pro Gly Arg Gly Ser Arg Pro Arg Ala Leu
108          400          405          410
109 Leu Glu Ala Pro Leu Lys Gln Ser Thr Phe Thr Leu Pro Leu Ser Asn
110          415          420          425

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```

111 Gln Leu Ala Ser Val Asn Pro Ser Leu Val Lys Val His Ile His His
112 430                      435                      440                      445
113 Pro Pro Glu Ala Ser Val Gln Ile His Gln Val Ala Gln Val Arg Gly
114                      450                      455                      460
115 Gly Val Glu Glu Ala Leu Val Glu Asn Ser Val Glu Thr Arg Pro Pro
116                      465                      470                      475
117 Pro Trp Leu Pro Ala Ser Pro Gly His Ser Leu Trp Asp Ser Asn Asn
118                      480                      485                      490
119 Ile Pro Ala Arg Ser Gly Glu Pro Pro Arg Pro Leu Pro Pro Ala Ala
120                      495                      500                      505
121 Pro Arg Pro Arg Gly Leu Leu Gly Arg Cys Tyr Leu Asn Thr Val Asn
122 510                      515                      520                      525
123 Gly Gln Cys Ala Asn Pro Leu Leu Glu Leu Thr Thr Gln Glu Asp Cys
124                      530                      535                      540
125 Cys Gly Ser Val Gly Ala Phe Trp Gly Val Thr Leu Cys Ala Pro Cys
126                      545                      550                      555
127 Pro Pro Arg Pro Ala Ser Pro Val Ile Glu Asn Gly Gln Leu Glu Cys
128                      560                      565                      570
129 Pro Gln Gly Tyr Lys Arg Leu Asn Leu Thr His Cys Gln Asp Ile Asn
130                      575                      580                      585
131 Glu Cys Leu Thr Leu Gly Leu Cys Lys Asp Ala Glu Cys Val Asn Thr
132 590                      595                      600                      605
133 Arg Gly Ser Tyr Leu Cys Thr Cys Arg Pro Gly Leu Met Leu Asp Pro
134                      610                      615                      620
135 Ser Arg Ser Arg Cys Val Ser Asp Lys Ala Ile Ser Met Leu Gln Gly
136                      625                      630                      635
137 Leu Cys Tyr Arg Ser Leu Gly Pro Gly Thr Cys Thr Leu Pro Leu Ala
138                      640                      645                      650
139 Gln Arg Ile Thr Lys Gln Ile Cys Cys Cys Ser Arg Val Gly Lys Ala
140                      655                      660                      665
141 Trp Gly Ser Glu Cys Glu Lys Cys Pro Leu Pro Gly Thr Glu Ala Phe
142 670                      675                      680                      685
143 Arg Glu Ile Cys Pro Ala Gly His Gly Tyr Thr Tyr Ala Ser Ser Asp
144                      690                      695                      700
145 Ile Arg Leu Ser Met Arg Lys Ala Glu Glu Glu Glu Leu Ala Arg Pro
146                      705                      710                      715
147 Pro Arg Glu Gln Gly Gln Arg Ser Ser Gly Ala Leu Pro Gly Pro Ala
148                      720                      725                      730
149 Glu Arg Gln Pro Leu Arg Val Val Thr Asp Thr Trp Leu Glu Ala Gly
150                      735                      740                      745
151 Thr Ile Pro Asp Lys Gly Asp Ser Gln Ala Gly Gln Val Thr Thr Ser
152 750                      755                      760                      765
153 Val Thr His Ala Pro Ala Trp Val Thr Gly Asn Ala Thr Thr Pro Pro
154                      770                      775                      780
155 Met Pro Glu Gln Gly Ile Ala Glu Ile Gln Glu Glu Gln Val Thr Pro
156                      785                      790                      795
157 Ser Thr Asp Val Leu Val Thr Leu Ser Thr Pro Gly Ile Asp Arg Cys
158                      800                      805                      810
159 Ala Ala Gly Ala Thr Asn Val Cys Gly Pro Gly Thr Cys Val Asn Leu

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```

160      815      820      825
161 Pro Asp Gly Tyr Arg Cys Val Cys Ser Pro Gly Tyr Gln Leu His Pro
162 830      835      840      845
163 Ser Gln Ala Tyr Cys Thr Asp Asp Asn Glu Cys Leu Arg Asp Pro Cys
164      850      855      860
165 Lys Gly Lys Gly Arg Cys Ile Asn Arg Val Gly Ser Tyr Ser Cys Phe
166      865      870      875
167 Cys Tyr Pro Gly Tyr Thr Leu Ala Thr Ser Gly Ala Thr Gln Glu Cys
168      880      885      890
169 Gln Asp Ile Asn Glu Cys Glu Gln Pro Gly Val Cys Ser Gly Gly Gln
170      895      900      905
171 Cys Thr Asn Thr Glu Gly Ser Tyr His Cys Glu Cys Asp Gln Gly Tyr
172 910      915      920      925
173 Ile Met Val Arg Lys Gly His Cys Gln Asp Ile Asn Glu Cys Arg His
174      930      935      940
175 Pro Gly Thr Cys Pro Asp Gly Arg Cys Val Asn Ser Pro Gly Ser Tyr
176      945      950      955
177 Thr Cys Leu Ala Cys Glu Glu Gly Tyr Arg Gly Gln Ser Gly Ser Cys
178      960      965      970
179 Val Asp Val Asn Glu Cys Leu Thr Pro Gly Val Cys Ala His Gly Lys
180      975      980      985
181 Cys Thr Asn Leu Glu Gly Ser Phe Arg Cys Ser Cys Glu Gln Gly Tyr
182 990      995      1000      1005
183 Glu Val Thr Ser Asp Glu Lys Gly Cys Gln Asp Val Asp Glu Cys Ala
184      1010      1015      1020
185 Ser Arg Ala Ser Cys Pro Thr Gly Leu Cys Leu Asn Thr Glu Gly Ser
186      1025      1030      1035
187 Phe Ala Cys Ser Ala Cys Glu Asn Gly Tyr Trp Val Asn Glu Asp Gly
188      1040      1045      1050
189 Thr Ala Cys Glu Asp Leu Asp Glu Cys Ala Phe Pro Gly Val Cys Pro
190      1055      1060      1065
191 Ser Gly Val Cys Thr Asn Thr Ala Gly Ser Phe Ser Cys Lys Asp Cys
192 1070      1075      1080      1085
193 Asp Gly Gly Tyr Arg Pro Ser Pro Leu Gly Asp Ser Cys Glu Asp Val
194      1090      1095      1100
195 Asp Glu Cys Glu Asp Pro Gln Ser Ser Cys Leu Gly Gly Glu Cys Lys
196      1105      1110      1115
197 Asn Thr Val Gly Ser Tyr Gln Cys Leu Cys Pro Gln Gly Phe Gln Leu
198      1120      1125      1130
199 Ala Asn Gly Thr Val Cys Glu Asp Val Asn Glu Cys Met Gly Glu Glu
200      1135      1140      1145
201 His Cys Ala Pro His Gly Glu Cys Leu Asn Ser His Gly Ser Phe Phe
202 1150      1155      1160      1165
203 Cys Leu Cys Ala Pro Gly Phe Val Ser Ala Glu Gly Gly Thr Ser Cys
204      1170      1175      1180
205 Gln Asp Val Asp Glu Cys Ala Thr Thr Asp Pro Cys Val Gly Gly His
206      1185      1190      1195
207 Cys Val Asn Thr Glu Gly Ser Phe Asn Cys Leu Cys Glu Thr Gly Phe
208      1200      1205      1210

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```

209 Gln Pro Ser Pro Glu Ser Gly Glu Cys Val Asp Ile Asp Glu Cys Glu
210      1215      1220      1225
211 Asp Tyr Gly Asp Pro Val Cys Gly Thr Trp Lys Cys Glu Asn Ser Pro
212 1230      1235      1240      1245
213 Gly Ser Tyr Arg Cys Val Leu Gly Cys Gln Pro Gly Phe His Met Ala
214      1250      1255      1260
215 Pro Asn Gly Asp Cys Ile Asp Ile Asp Glu Cys Ala Asn Asp Thr Met
216      1265      1270      1275
217 Cys Gly Ser His Gly Phe Cys Asp Asn Thr Asp Gly Ser Phe Arg Cys
218      1280      1285      1290
219 Leu Cys Asp Gln Gly Phe Glu Ile Ser Pro Ser Gly Trp Asp Cys Val
220      1295      1300      1305
221 Asp Val Asn Glu Cys Glu Leu Met Leu Ala Val Cys Gly Ala Ala Leu
222 1310      1315      1320      1325
223 Cys Glu Asn Val Glu Gly Ser Phe Leu Cys Leu Cys Ala Ser Asp Leu
224      1330      1335      1340
225 Glu Glu Tyr Asp Ala Gln Glu Gly His Cys Arg Pro Arg Gly Ala Gly
226      1345      1350      1355
227 Gly Gln Ser Met Ser Glu Ala Pro Thr Gly Asp His Ala Pro Ala Pro
228      1360      1365      1370
229 Thr Arg Met Asp Cys Tyr Ser Gly Gln Lys Gly His Ala Pro Cys Ser
230      1375      1380      1385
231 Ser Val Leu Gly Arg Asn Thr Thr Gln Ala Glu Cys Cys Cys Thr Gln
232 1390      1395      1400      1405
233 Gly Ala Ser Trp Gly Asp Ala Cys Asp Leu Cys Pro Ser Glu Asp Ser
234      1410      1415      1420
235 Ala Glu Phe Ser Glu Ile Cys Pro Ser Gly Lys Gly Tyr Ile Pro Val
236      1425      1430      1435
237 Glu Gly Ala Trp Thr Phe Gly Gln Thr Met Tyr Thr Asp Ala Asp Glu
238      1440      1445      1450
239 Cys Val Ile Phe Gly Pro Gly Leu Cys Pro Asn Gly Arg Cys Leu Asn
240      1455      1460      1465
241 Thr Val Pro Gly Tyr Val Cys Leu Cys Asn Pro Gly Phe His Tyr Asp
242 1470      1475      1480      1485
243 Ala Ser His Lys Lys Cys Glu Asp His Asp Glu Cys Gln Asp Leu Ala
244      1490      1495      1500
245 Cys Glu Asn Gly Glu Cys Val Asn Thr Glu Gly Ser Phe His Cys Phe
246      1505      1510      1515
247 Cys Ser Pro Pro Leu Thr Leu Asp Leu Ser Gln Gln Arg Cys Met Asn
248      1520      1525      1530
249 Ser Thr Ser Ser Thr Glu Asp Leu Pro Asp His Asp Ile His Met Asp
250      1535      1540      1545
251 Ile Cys Trp Lys Lys Val Thr Asn Asp Val Cys Ser Glu Pro Leu Arg
252 1550      1555      1560      1565
253 Gly His Arg Thr Thr Thr Glu Cys Cys Gln Asp Gly Glu Ala
254      1570      1575      1580
255 Trp Ser Gln Gln Cys Ala Leu Cys Pro Pro Arg Ser Ser Glu Val Tyr
256      1585      1590      1595
257 Ala Gln Leu Cys Asn Val Ala Arg Ile Glu Ala Glu Arg Glu Ala Gly

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VERIFICATION SUMMARY

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PATENT APPLICATION: US/10/519,328

TIME: 12:28:45

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\02242006\J519328.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:48 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:52 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1